

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 13:23:34 ; Search time 2659.16 Seconds
(without alignments)
4224.860 Million cell updates/sec

Title: US-09-602-833A-3
Perfect score: 681
Sequence: 1 atgagaattctgagctgcgc.....ctttagccttcaacttga 681

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1472140 segs, 8248589755 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_ov:*
7: gb_ov:*
8: gb_ov:*
9: gb_ov:*
10: gb_ov:*
11: gb_ov:*
12: gb_ov:*
13: gb_ov:*
14: gb_ov:*
15: gb_ov:*
16: gb_ov:*
17: gb_ov:*
18: gb_ov:*
19: gb_ov:*
20: gb_ov:*
21: gb_ov:*
22: gb_ov:*
23: gb_ov:*
24: gb_ov:*
25: gb_ov:*
26: gb_ov:*
27: gb_ov:*
28: gb_ov:*
29: gb_ov:*
30: gb_ov:*
31: gb_ov:*
32: gb_ov:*
33: gb_ov:*
34: gb_ov:*
35: gb_ov:*
36: gb_ov:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	681	100.0	681	6	AX063234	AX063234 Sequence
2	681	100.0	1116	6	AX063232	AX063232 Sequence
3	681	100.0	4860	9	HSAB08569	AJ308569 Homo sapi
4	158	23.2	145795	2	HSAB310996	AJ310996 Homo sapi
5	158	23.2	202324	2	AC068720	AC068720 Homo sapi
6	137	20.1	202324	2	AC068720	AC068720 Homo sapi
7	129	18.9	2056	9	AK021919	AK021919 Homo sapi
8	36	5.3	172866	9	AC013467	AC013467 Homo sapi
9	22	3.2	153929	3	AC025574	AC025574 Homo sapi
10	21	3.1	77644	3	AC090521	AC090521 Caenorhab
11	21	3.1	109549	2	AC001181	AC001181 Homo sapi
12	21	3.1	163332	9	AC004821	AC004821 Homo sapi
13	21	3.1	180541	2	AC016521	AC016521 Homo sapi
14	21	3.1	193379	2	AC022182	AC022182 Homo sapi
15	20	2.9	410	1	RP282365	Z82365 R. prowazeki
16	20	2.9	982	5	S7292353	S72923 xenopus lae
17	20	2.9	1076	5	XLENK02	X00853 proenkephal
18	20	2.9	1359	5	XLENK01	X00852 Xenopus lae
19	20	2.9	38749	3	AF099001	AF099001 Caenorhab
20	20	2.9	73174	2	AC036161	AC036161 Homo sapi
21	20	2.9	95397	8	AC007112	AC007112 Arabidops
22	20	2.9	103219	2	AC007945	AC007945 Homo sapi
23	20	2.9	139480	2	AC012837	AC012837 Drosophi
24	20	2.9	147160	2	AC010047	AC010047 Drosophi
25	20	2.9	160264	9	AL442644	AL442644 Human DNA
26	20	2.9	176174	9	AC007483	AC007483 Homo sapi
27	20	2.9	178429	2	AC026462	AC026462 Homo sapi
28	20	2.9	181360	2	AL356072	AL356072 Homo sapi
29	20	2.9	183457	2	AC092420	AC092420 Homo sapi
30	20	2.9	187215	33	AC068761	AC068761 Homo sapi
31	20	2.9	189287	2	AC068362	AC068362 Homo sapi
32	20	2.9	195959	2	AC034143	AC034143 Homo sapi
33	20	2.9	198254	9	AC016049	AC016049 Homo sapi
34	20	2.9	200918	9	AC012360	AC012360 Homo sapi
35	20	2.9	209058	10	AC079181	AC079181 Mus muscu
36	20	2.9	249433	2	AC051620	AC051620 Mus muscu
37	20	2.9	309883	3	AE003479	AE003479 Drosophi
38	19	2.8	548	9	HSBFF244S1	U21911 Human basic
39	19	2.8	860	9	BC005345	BC005345 Homo sapi
40	19	2.8	1185	6	A47122	A47122 Sequence 3
41	19	2.8	1185	9	HSBFF244K	Z30094 H.sapiens B
42	19	2.8	2010	4	SSP2A55A	Z34932 S.scrofa mr
43	19	2.8	2034	8	AF370515	AF370515 Arabidops
44	19	2.8	2037	8	AFH245414	AJ245414 Arabidops
45	19	2.8	3071	10	AF254070	AF254070 Mus muscu

ALIGNMENTS

RESULT	1	LOCUS	AX063234	DEFINITION	Sequence 3 from Patent WO0078959.	PAT	24-JAN-2001
AX063234	LOCUS	AX063234	681 bp	DNA			
AX063234	DEFINITION	Sequence 3 from Patent WO0078959.					
AX063234	ACCESSION	AX063234					
AX063234.1	VERSION	GI:12541060					
AX063234.1	KEYWORDS						
AX063234.1	SOURCE	human.					
AX063234.1	ORGANISM	Homo sapiens					
AX063234.1	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AX063234.1	AUTHORS	Turner,A.C., Zambrowicz,B., Nehls,M., Friedrich,G.A. and Sands,A.T.					
AX063234.1	TITLE	Human genes and proteins encoded thereby					
AX063234.1	JOURNAL	Patent: WO 0078959-A 3 28-DIC-2000;					
AX063234.1	FEATURES	Lexicon Genetics Incorporated (US)					
AX063234.1	source	Location/Qualifiers					
AX063234.1	source	1..681					
AX063234.1	source	/organism="Homo sapiens"					
AX063234.1	source	/db_xref="taxon:9606"					

CDS	1..681	/note="unnamed protein product"
	/codon_start=1	
	/protein_id="CAC25078.1"	
	/db_xref="GI:12541061"	
	/translation="MRILDPKNDISLPAEIGIKLNKELANGFNKLSIPPELGC ENLRDSCGNLELPELISNKOYFVIDISANKSSVPICVLRNSLNQMDISSN NLPDLPODIDRELEOSFLYKRNKLYLPYSMLNKKLTLLVSGDLVELPTALCDS STPLKFEVSLMDNPIDNACEDGNEIMESERDHFDEKVKAVIEDLKERESVPSYTT KVSFSLQ"	
BASE COUNT	212 a 138 c 142 g 189 t	
ORIGIN		
Query Match	100.0%;	Score 681; DB 6; Length 681;
Best Local Similarity	100.0%;	Pred. No. 0;
Matches 681; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Oy	1 atgagaattctggaatcgcgaacaaacaaatctcaactctccagcagaatcggtgtc	60
Db	1 ATGGAATTCTGGATCTGCCAAAAACCAATCTCACATCTCCAGCGAAATCGGTTGT	60
Oy	61 ttgagaacctggaagaactcaatgtgttcaactctgaagagcattccctccagaa	120
Db	61 TTGAAGAACTGAAAGAACTCAATGTGGTTTCAACTATCTGAAGAGCATTCCTCGAAA	120
Oy	121 ttggagattgtgaatactagagagactgtgttcttggaactctagaatlaatgag	180
Db	121 TTGGAGATTGTGAAATCTAGAGAGACTGATGTTCTGAAATCTGAATTAATGAG	180
Oy	181 ctgacctttggaatgaagaattgaagaattgaattgtgaattgtgaattgtgaagaag	240
Db	181 CTGCCCTTGAATTGAATTTGAAGCAAGTTACATTGTGAGATATCTGACCAACAG	240
Oy	241 ttcccaagtcgccaactctgtctcgtcggaatgcgaattctgagttgttgatacagc	300
Db	241 TTTTCCAGTGTCCCAATGTGTCTCGGATGTGATTTGCAAGTGTGTGATATCAGC	300
Oy	301 agcaataacctgaccgacctgcgcaagataagaagctagaggctgcagaagcttc	360
Db	301 AGCAATAACCTGACCGACCTGCCCAAGATATGACAGGCTAGAGACCTGCAGAGCTTT	360
Oy	361 ctctgtataaacaagttaacttaacttaacttaacttaacttaacttaacttaactta	420
Db	361 CTCTGTATATAAACAAGTTGACTTACCTTCCCTATTCACATGCTGAACCTGAAGAGCTC	420
Oy	421 actctgttagtcgctcagtgaggacatttggtagagctcccaactgaccttctgagctca	480
Db	421 ACTCTGTAGTCGTCAGTGGGGACCAATTGGTGGAGCTCCCAAGTCCCTTTGTGACTCA	480
Oy	481 tcgaacctttaaaattgttaagcctatggaacaactctatgataatgcccgaatgtgaa	540
Db	481 TCCACACCTTTAAATTTGTAAAGCTTATGGAATCTTATGATTAAGCCCAATGTGAA	540
Oy	541 gatggcaatgaataatgaagaatgaagaagctgagcgaacttttgataaagaagttag	600
Db	541 GATGGCAATGAATAATGAAGAATGAAGGAGATGCCCAACTTTTGTATTAAGAACTTATG	600
Oy	601 aaagcctatatctgaagaccttaagaagaagaatctgttccagctatataccaaccaagtg	660
Db	601 AAAGCCTATATTGAAGACCTTAAGAAAGAGAATCTGTCCAGACTATACCAACCAAGTG	660
Oy	661 tcttttagcctcaacttga 681	
Db	661 TCTTTAGCCTTCAACTTTGA 681	
RESULT 2		
LOCUS	AX063232	1116 bp DNA
DEFINITION	Sequence 1 from Patent WO0078959.	PAT
ACCESSION	AX063232	
VERSION	AX063232.1	GI:12541058

KEYWORDS	human.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 1116)
AUTHORS	Turner,A.C., Zambrowicz,B., Nehls,M., Friedrich,G.A. and Sands,A.T.
TITLE	Human genes and proteins encoded thereby
JOURNAL	Patent: WO 0078959-A 1 28-DEC-2000; Lexicon Genetics Incorporated (US)
FEATURES	Location/Qualifiers
SOURCE	1..1116
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
CDS	1..1116
	/note="unnamed protein product"
	/codon_start=1
	/protein_id="CAC25077.1"
	/db_xref="GI:12541059"
	/translation="MGKVVYFDISVLRALMERYKKHKKAMOKKEVERLEKSALEKIK EEMNVEACRRKGIPOAVYCNKGFIDTSVRLDKIERNTLROSLLPDKRKSATFV FELSGEHWTELPDLKEDTHLREWIYISNTLOIIPYIOLPQAMRILDPKNOISHP AEIGLKNLELNGFVYKLSIPPELDCENLELDCSNLELPELPELISNKOYF VDISANKSSVPICVLRNSLNQMDISSNNLTDLPODIDRELEOSFLYKRNKLYLP YSMLNKKLTLLVSGDHLVELPTALCDSSTPLKFEVSLMDNPIDNACEDGNEIMESE RDRHFDEKVKAVIEDLKERESVPSYTTKVSFSLQ"
BASE COUNT	343 a 224 c 265 g 284 t
ORIGIN	
Query Match	100.0%; Score 681; DB 6; Length 1116;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 681; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 atgagaattctggaatcgcgaacaaacaaatctcaactctccagcagaatcggtgtc 60
Db	436 ATGGAATTCTGGATCTGCCAAAAACCAATCTCACATCTCCAGCGAAATCGGTTGT 495
OY	61 ttgagaacctggaagaactcaatgtgttcaactctgaagagcattccctccagaa 120
Db	496 TTGAAGAACTGAAAGAACTCAATGTGGTTTCAACTATCTGAAGAGCATTCCTCGAAA 555
OY	121 ttggagattgtgaatactagagagactgtgttcttggaactctagaatlaatgag 180
Db	556 TTGGAGATTGTGAAATCTAGAGAGACTGATTTGTGGAATCTGGAATTAATGAG 615
OY	181 ctgacctttgaatgaagaattgaagaagcttaacttctgagatatactcagaacaag 240
Db	616 CTGCCCTTGAATTGAATTTGAAGCAAGTTACTTGTGAGATATCTGACCAACAG 675
OY	241 ttcccaagtcgccaactctgtctcgtcggaatgcgaattctgagttgttgatacagc 300
Db	676 TTTTCCAGTGTGCCCAATGTGTCTCGGATGTGGAATTTGCAATGTGGATATCAGC 735
OY	301 agcaataacctgaccgacctgcgcaagataagaagctagaggctgcagaagcttc 360
Db	736 AGCAATAACCTGACCGACCTGCCAAGATATGACAGGCTAGAGAGACTGCAGAGCTTT 795
OY	361 ctctgtataaacaagttaacttaacttaacttaacttaacttaacttaacttaactta 420
Db	796 CTCTGTATATAAACAAGTTGACTTACCTTCCCTATTCACATGCTGAACCTGAAGAGCTC 855
OY	421 actctgttagtcgctcagtgaggacatttggtagagctcccaactgaccttctgagctca 480
Db	856 ACTCTGTAGTCGTCAGTGGGGACCAATTGGTGGAGCTCCCAACTGCTTTGTGACTCA 915
OY	481 tcgaacctttaaaattgttaagcctatggaacaactctatgataatgcccgaatgtgaa 540
Db	916 TCCACACCTTTAAATTTGTAAAGCTTATGGAATCTTATGATTAAGCCCAATGTGAA 975
OY	541 gatggcaatgaataatgaagaatgaagaagctgagcgaacttttgataaagaagttag 600
Db	976 GATGGCAATGAATAATGAAGAATGAAGGAGATGCCCAACTTTTGAATTAAGAAATGATG 1035

QY 601 aaagcctataatgaagccttaagaaagaatctgttccaccatacaccagaagt 660
|||||
Db 1036 AAGCGATATGTGAAGACCTTAAGAAGAAAGAAATCTGTCCACCTTACCACCAAGT 1095
QY 661 tctttaagcctcaacttga 681
|||||
Db 1096 TCTTTAGCCTTCAACTTGA 1116
|||||
RESULT 3
HSA308569 4860 bp mRNA PRI 06-JUN-2001
LOCUS Homo sapiens mRNA for leucine-rich repeat-containing 2 protein
DEFINITION (LRRC2 gene).
ACCESSION AJ308569.2 GI:14330408
VERSION AJ308569.2 GI:14330408
KEYWORDS leucine-rich repeat-containing 2 protein; LRRC2 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 4860)
AUTHORS Kiss, H., Yang, Y., Kost-Alimova, M., Szeles, A., Kholodnyuk, I.,
Kedra, D., Kiss, C., Klein, G., Imreh, S. and Dumanaki, J.P.
TITLE Transcriptional map of the Common Eliminated Region 1 on human
3p21.3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4860)
AUTHORS Kiss, H.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2001) Kiss H., Microbiology and Tumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN
REMARK Revised by [3]
REFERENCE 3 (bases 1 to 4860)
AUTHORS Kiss, H.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2001) Kiss H., Microbiology and Tumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN
COMMENT On Jun 8, 2001 this sequence version replaced gi:13186111.
FEATURES
source
location/Qualifiers
1..4860
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21.3"
168..1283
/gene="LRRC2"
168..1283
/gene="LRRC2"
/codon_start=1
/product="leucine-rich repeat-containing 2 protein"
/protein_id="CAC33442.1"
/db_xref="GI:13186112"
/translation="MGKVVVFDISVIRALMTRVKKHAKMOKKEVERLEKSALEKIK
EEMNFVAFBCRRKGIPOAGYCKNGFIDFSVLDIKIRNLTROSSLPKDGKSSAFV
FELSGHWTELPDPSLEKEQTHLRMYISNTLIOTIPIYIQLFQMRILDPKNOISHP
AETGLKLNKELWGFNYLKTIPPELGDCENLRDSCGLMELEPFEISLNKQVTF
VLSANKFSSVPCIVLRMSNLQWLDISSNNLTDLDPDIDLELQSFLLYKNLTLP
YSMLNKTLLIVVSGDHLVELPTALCDSSTPLKFEVSLMDNPIDNAQCEDEGNEIMSE
RDRQHEDEKVMKVIIDLEKRESVPTTKVSPSLQ"
BASE COUNT 1480 a 924 c 1162 g 1294 t
ORIGIN
Query Match 100.0%; Score 681; DB 9; Length 4860;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 603 ATGAGAAATTCGTGATCTGCCAAAAAACCAATCTCACATCTTCAGCAGAAATCGGTGT 662
QY 61 ttgaagaacctgaagaactcaatctgtggttcaactatctgaagagactctccagaa 120
|||||
Db 663 TTGAAGAACCCTGAAGAAGAACTCAATGTGGTTCAACTATCTGAAGAGCATTCCTCCAGAA 722
QY 121 ttggagaatctgaaatctagaagagactgattgttctggaatctagaatgaatgag 180
|||||
Db 723 TTGGAGATGTGAAAATCTAGAGAGACTGATGTGTTCTGGAATCTAGATTAATGAGAG 782
QY 181 ctgccttgaatgaatgaatctgaagcaagttcattctagatatctcagaacaag 240
|||||
Db 783 CTGCCCTTGAATTAAGAAATTTGAAGCAAGTTACATTTGATGATATCTCAGCAAAAG 842
QY 241 ttccagatgcccactgtgtctgtgagtgatgaggaattgacagtggttgatatagc 300
|||||
Db 843 TTTTCCAGTGTCCCAATCTGTCTCGGATGTGGAATTTGCAATGTTGATATCTCAGC 902
QY 301 agcaataacctgacacctgcgcgaagataagacagctagagagctgacagctt 360
|||||
Db 903 AGCATATACTGACCGACGACCTCCGCAAGATATAGACAGCGCTAGAGAGCTCAGAGCTTT 962
QY 361 ctcttgataaacaagttgaacctaccctccattccatgctgaactgaagaagctc 420
|||||
Db 963 CTCTGTGATAAACAAGTTGACCTACCTTCCTATTCCATGCACTGAACCTGAAGAAGCTC 1022
QY 421 actctgtatgctgcagtgaggagacattgtgtgagctcccaactgacctgtgaccca 480
|||||
Db 1023 ACTCTGTAGTGTGACGAGGGGACCATTTGTTGAGCTCCCACTGCCCTTTGTGACCA 1082
QY 481 tccacaccttaaatctgtgaagccttaagacaatccattgataatgcccactgttaa 540
|||||
Db 1083 TCCACACCTTAAATTTGTGAAGCTTATGACATCTATGTAATAGCCCAATGTGAA 1142
QY 541 gatggcaatgaataatgaagaaatgaacggagatgcgaacatttgataaagaagtac 600
|||||
Db 1143 GATGGCAATGAATAATGAGAAAGTGAACGGATGCCCAATTTGTGATAAAGAAAGTATG 1202
QY 601 aaagcctataatgaagccttaagaaagaatctgttccaccatacaccagaagt 660
|||||
Db 1203 AAGCGATATGTGAAGACCTTAAGAAGAAAGAAATCTGTCCACCTTACCACCAAGT 1262
QY 661 tctttaagcctcaacttga 681
|||||
Db 1263 TCTTTAGCCTTCAACTTGA 1283
|||||
RESULT 4
HSA310996/c 145795 bp DNA HTG 18-APR-2001
LOCUS Homo sapiens chromosome 3 clone RP6-91P17 map 3p21.3. ***
DEFINITION SEQUENCING IN PROGRESS ***, 42 ordered pieces.
ACCESSION AJ310996
VERSION AJ310996.1 GI:13751170
KEYWORDS HTG; HTGS_PHASE2.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 145795)
AUTHORS Kiss, H., Yang, Y., Kost-Alimova, M., Szeles, A., Kholodnyuk, I.,
Kedra, D., Kiss, C., Klein, G., Imreh, S. and Dumanaki, J.P.
TITLE Transcriptional map of the common eliminated region 1 on human
3p21.3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 145795)
AUTHORS Kiss, H.
TITLE Direct Submission
JOURNAL Submitted (17-APR-2001) Kiss H., Microbiology and Tumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN
COMMENT The sequencing contigs are in order and the gaps between them are
represented by 100 n's.

Contig 1: 1-2508 Contig 2: 2609-17434 Contig 3: 17535-21987
 Contig 4: 22088-23066 Contig 5: 23167-28845 Contig 8:
 Contig 6: 28946-30840 Contig 7: 30941-37879
 37980-38928 Contig 9: 39029-40834 Contig 10: 40935-44527 Contig
 11: 44628-48077 Contig 12: 48178-52755 Contig 13: 52856-53293
 Contig 14: 53394-54768 Contig 15: 54869-57895 Contig 16:
 57996-59322 Contig 17: 59423-60159 Contig 18: 60260-61231
 Contig 19: 61332-62928 Contig 20: 63029-63852 Contig 21:
 63953-75555 Contig 22: 75656-77760 Contig 23: 77861-79686
 87723-89164 Contig 27: 89265-90007 Contig 28: 90108-92035
 Contig 29: 92136-97298 Contig 30: 97399-102032 Contig 31:
 102133-106605 Contig 32: 106706-108263 Contig 33: 108364-110022
 Contig 34: 110123-113747 Contig 35: 113848-125151 Contig 36:
 125252-126026 Contig 37: 126127-129649 Contig 38: 129750-132160
 Contig 39: 132261-133125 Contig 40: 133226-135661 Contig 41:
 135763-142148 Contig 42: 142249-145795.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 42 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 2508: contig of 2508 bp in length
 * 2509 2608: gap of 100 bp
 * 2609 17434: contig of 14826 bp in length
 * 17435 17534: gap of 100 bp
 * 17535 21987: contig of 4453 bp in length
 * 21988 22087: gap of 100 bp
 * 22088 23066: contig of 979 bp in length
 * 23067 23166: gap of 100 bp
 * 23167 28845: contig of 5679 bp in length
 * 28846 28945: gap of 100 bp
 * 28946 30840: contig of 1895 bp in length
 * 30841 30940: gap of 100 bp
 * 30941 37879: contig of 6939 bp in length
 * 37880 37979: gap of 100 bp
 * 37980 38928: contig of 949 bp in length
 * 38929 39028: gap of 100 bp
 * 39029 40834: contig of 1806 bp in length
 * 40835 40934: gap of 100 bp
 * 40935 44527: contig of 3593 bp in length
 * 44528 44627: gap of 100 bp
 * 44628 48077: contig of 3450 bp in length
 * 48078 48177: gap of 100 bp
 * 48178 52755: contig of 4578 bp in length
 * 52756 52855: gap of 100 bp
 * 52856 53293: contig of 438 bp in length
 * 53294 53393: gap of 100 bp
 * 53394 54768: contig of 1375 bp in length
 * 54769 54868: gap of 100 bp
 * 54869 57895: contig of 3027 bp in length
 * 57896 57995: gap of 100 bp
 * 57996 59322: contig of 1327 bp in length
 * 59323 59422: gap of 100 bp
 * 59423 60159: contig of 737 bp in length
 * 60160 60259: gap of 100 bp
 * 60260 61231: contig of 972 bp in length
 * 61232 61331: gap of 100 bp
 * 61332 62928: contig of 1597 bp in length
 * 62929 63028: gap of 100 bp
 * 63029 63852: contig of 824 bp in length
 * 63853 63952: gap of 100 bp
 * 63953 75555: contig of 11603 bp in length
 * 75556 75655: gap of 100 bp
 * 75656 77760: contig of 2105 bp in length
 * 77761 77860: gap of 100 bp
 * 77861 79686: contig of 1826 bp in length
 * 79687 79786: gap of 100 bp
 * 79787 80857: contig of 1071 bp in length

* 80858 80957: gap of 100 bp
 * 80958 87622: contig of 6665 bp in length
 * 87623 87722: gap of 100 bp
 * 87723 89164: contig of 1442 bp in length
 * 89165 89264: gap of 100 bp
 * 89265 90007: contig of 743 bp in length
 * 90008 90107: gap of 100 bp
 * 90108 92035: contig of 1928 bp in length
 * 92036 92135: gap of 100 bp
 * 92136 97298: contig of 5163 bp in length
 * 97299 97398: gap of 100 bp
 * 97399 102032: contig of 4634 bp in length
 * 102033 102132: gap of 100 bp
 * 102133 106605: contig of 4473 bp in length
 * 106606 106705: gap of 100 bp
 * 106706 108263: contig of 1558 bp in length
 * 108264 108363: gap of 100 bp
 * 108364 110022: contig of 1659 bp in length
 * 110023 110122: gap of 100 bp
 * 110123 113747: contig of 3625 bp in length
 * 113748 113847: gap of 100 bp
 * 113848 125151: contig of 11304 bp in length
 * 125152 125251: gap of 100 bp
 * 125252 126026: contig of 775 bp in length
 * 126027 126126: gap of 100 bp
 * 126127 129649: contig of 3523 bp in length
 * 129650 129749: gap of 100 bp
 * 129750 132160: contig of 2411 bp in length
 * 132161 132260: gap of 100 bp
 * 132261 133125: contig of 865 bp in length
 * 133126 133225: gap of 100 bp
 * 133226 135661: contig of 2436 bp in length
 * 135662 135761: gap of 100 bp
 * 135762 142148: contig of 6387 bp in length
 * 142149 142248: gap of 100 bp
 * 142249 145795: contig of 3547 bp in length.
 * Location/Qualifiers
 1. 145795
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="3"
 /map="3p21.3"
 /clone="Rpe-91P17"

BASE COUNT 39764 a 33207 c 31499 g 37225 t 4100 others
 ORIGIN

Query Match 23.2%: Score 158; DB 2: Length 145795;
 Best Local Similarity 100.0%; Pred. No. 2e-76;
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 337 aggcctagagagctgcagaagcttctctgtataaacaagttgacctaccctccat 396
 |||||||
 DB 61617 AGGCTAGAGAGAGCTGCAGAGCTTCTCTGTATATAAACAAGTTACCTGCTCCAT 61558
 |||||||
 OY 397 tccatctgtaacctgaagaagctcaactctgttagtcgtcagtgaggaccattggtgag 456
 |||||||
 DB 61557 TCcATGCTGAACCTGAAGAAGCTCACTGTAGTCGTACAGGCGACCATTTGGTGAG 61498
 |||||||
 OY 457 ctcccaactgccccttctgtgactcattccacaccttaaa 494
 |||||||
 DB 61497 CTCcCAACTGCCCTTTGTGACTCATCACACCTTTAAA 61460
 |||||||

RESULT 5
 AC068720 AC068720 202324 bp DNA HTG 07-JUL-2000
 LOCUS Homo sapiens chromosome 3 clone RP11-509121, WORKING DRAFT
 DEFINITION
 SEQUENCE, 20 unordered pieces.
 AC068720 AC068720 2 GI:8469022
 VERSION
 KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 202324)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 202324)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jun 12, 2000 this sequence version replaced gi:7715661.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0509121
----- Summary Statistics -----
Sequencing vector: M13; 1008
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 193150 bases at least Q40
Consensus quality: 193686 bases at least Q30
Consensus quality: 197015 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 200424; sum-of-contigs
Quality coverage: 4.67 in Q20 bases; agarose-fp
Quality coverage: 4.72 in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1576: contig of 1576 bp in length
* 1577 1676: gap of unknown length
* 1677 3263: contig of 1587 bp in length
* 3264 3363: gap of unknown length
* 3364 5443: contig of 2080 bp in length
* 5444 5543: gap of unknown length
* 5544 8196: contig of 2653 bp in length
* 8197 8296: gap of unknown length
* 8297 12038: contig of 3742 bp in length
* 12039 12138: gap of unknown length
* 12139 15992: contig of 3854 bp in length
* 15993 16092: gap of unknown length
* 16093 21192: contig of 5100 bp in length
* 21193 21292: gap of unknown length
* 21293 24766: contig of 3474 bp in length
* 24767 24866: gap of unknown length
* 24867 30824: contig of 5958 bp in length
* 30825 30924: gap of unknown length
* 30925 37153: contig of 6229 bp in length
* 37154 37253: gap of unknown length
* 37254 45262: contig of 8009 bp in length
* 45263 45362: gap of unknown length
* 45363 56733: contig of 11371 bp in length
* 56734 56833: gap of unknown length
* 56834 72156: contig of 15323 bp in length
* 72157 72256: gap of unknown length
* 72257 84702: contig of 12446 bp in length
* 84703 84802: gap of unknown length
* 84803 101052: contig of 16250 bp in length
* 101053 101152: gap of unknown length

FEATURES
source
1. .202324
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-509121"
1. .1576
/note="assembly_name:Contig4"
1677. .3263
/note="assembly_name:Contig5"
3364. .5443
/note="assembly_name:Contig6"
5544. .8196
/note="assembly_name:Contig7"
8297. .12038
/note="assembly_name:Contig8"
12139. .15992
/note="assembly_name:Contig9"
clone_end:77
vector_side:right"
16093. .21192
/note="assembly_name:Contig10"
21293. .24766
/note="assembly_name:Contig11"
24867. .30824
/note="assembly_name:Contig12"
30925. .37153
/note="assembly_name:Contig13"
37254. .45262
/note="assembly_name:Contig14"
45363. .56733
/note="assembly_name:Contig15"
56834. .72156
/note="assembly_name:Contig16"
72257. .84702
/note="assembly_name:Contig17"
84803. .101052
/note="assembly_name:Contig18"
101153. .117709
/note="assembly_name:Contig19"
117810. .132650
/note="assembly_name:Contig20"
clone_end:SP6
vector_side:left"
132751. .152071
/note="assembly_name:Contig21"
152172. .176190
/note="assembly_name:Contig22"
176291. .202324
/note="assembly_name:Contig23"

BASE COUNT 56787 a 45300 c 43765 g 54528 t 1944 others
ORIGIN

Query Match 23.28; Score 158; DB 2; Length 202324;
Best Local Similarity 100.0%; Pred. No. 2e-76;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ox 337 agcctagagagcgcgcagccttctcttataaacaagtgtacctaccctccat 396
|||||
Db 96876 AGCCTAAGAGAGCGCGAGACCTTCTCTGTATATAAACAAGTTGACCTTACCTTAT 96935
|||||
Ox 397 tccatgtgaacctgaagaagctcactctgttagctgctagtggtgaccatlgtgtgag 456
|||||

Db 96936 TCCATGCTGACCTGAGAGACTGCTGTTAGTCGTCATGGGACCATTTGGTGAG 96995
 Oy 457 ctcccaactgccttctgtgcatcacacaccttaaa 494
 Db 96996 CTCCTCACTGCGCTTTGTGATCATTCACACCTTTAAA 97033

RESULT 6
 AC068720/c AC068720 202324 bp DNA HTG 07-JUL-2000
 LOCUS Homo sapiens chromosome 3 clone RP11-509I21, WORKING DRAFT
 DEFINITION SEQUENCE, 20 unordered pieces.
 ACCESSION AC068720
 VERSION AC068720.2 GI:8469022
 KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 202324)
 AUTHORS Waterston,R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 202324)
 AUTHORS Waterston,R.H.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAY-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 COMMENT On Jun 12, 2000 this sequence version replaced gi:7715661.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H_NH0509121
 ----- Summary Statistics -----
 Sequencing vector: M13; 100%
 Sequencing vector: plasmid; 0%
 Chemistry: Dye-primer ET; 100% of reads
 Chemistry: Dye-terminator Big Dye; 0% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 193150 bases at least Q40
 Consensus quality: 195686 bases at least Q20
 Consensus quality: 197015 bases at least Q20
 Insert size: 200000; agarose-fp
 Insert size: 200424; sum-of-contigs
 Quality coverage: 4.67 in Q20 bases; agarose-fp
 Quality coverage: 4.72 in Q20 bases; sum-of-contigs
 ----- NOTE: This is a 'working draft' sequence. It currently
 * consists of 20 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1576: contig of 1576 bp in length
 * 1577 1676: gap of unknown length
 * 1677 3263: contig of 1587 bp in length
 * 3263 3363: gap of unknown length
 * 3363 3443: contig of 2080 bp in length
 * 3443 5443: gap of unknown length
 * 5443 5544: gap of unknown length
 * 5544 8197: contig of 2653 bp in length
 * 8197 8297: gap of unknown length
 * 8297 12038: contig of 3742 bp in length
 * 12038 12139: gap of unknown length
 * 12139 15992: contig of 3854 bp in length
 * 15992 16093: gap of unknown length
 * 16093 21192: contig of 5100 bp in length
 * 21192 21293: gap of unknown length

FEATURES
 source * 21293 24766: contig of 3474 bp in length
 * 24767 24866: gap of unknown length
 * 24867 30824: contig of 5958 bp in length
 * 30825 30925: gap of unknown length
 * 30925 37154: contig of 6229 bp in length
 * 37154 37253: gap of unknown length
 * 37253 45262: contig of 8009 bp in length
 * 45263 45363: gap of unknown length
 * 45363 56734: contig of 11371 bp in length
 * 56734 56834: gap of unknown length
 * 56834 72157: contig of 15323 bp in length
 * 72157 72257: gap of unknown length
 * 72257 84702: contig of 12446 bp in length
 * 84703 84803: gap of unknown length
 * 84803 101052: contig of 16250 bp in length
 * 101053 101153: gap of unknown length
 * 101153 117710: contig of 16557 bp in length
 * 117710 117810: gap of unknown length
 * 117810 132651: contig of 14841 bp in length
 * 132651 132751: gap of unknown length
 * 132751 152071: contig of 19321 bp in length
 * 152072 152172: gap of unknown length
 * 152172 176191: contig of 24019 bp in length
 * 176191 176291: gap of unknown length
 * 176291 202324: contig of 26034 bp in length.

Location/Qualifiers
 1..202324
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="3"
 /clone="RP11-509I21"
 1..1576
 /note="assembly_name:Contig4"
 1677..3263
 /note="assembly_name:Contig5"
 3364..5443
 /note="assembly_name:Contig6"
 5444..8196
 /note="assembly_name:Contig7"
 8297..12038
 /note="assembly_name:Contig8"
 12139..15992
 /note="assembly_name:Contig9
 /note="assembly_name:Contig10"
 16093..21192
 /note="assembly_name:Contig11"
 21293..24766
 /note="assembly_name:Contig12"
 24867..30824
 /note="assembly_name:Contig13"
 30925..37153
 /note="assembly_name:Contig14"
 37254..45262
 /note="assembly_name:Contig15"
 45363..56733
 /note="assembly_name:Contig16"
 56834..72156
 /note="assembly_name:Contig17"
 72257..84702
 /note="assembly_name:Contig18"
 84803..101052
 /note="assembly_name:Contig19"
 101153..117709
 /note="assembly_name:Contig20"
 117810..132650
 /note="assembly_name:Contig21"
 132751..152071
 /note="assembly_name:Contig22"
 152172..176190
 /note="assembly_name:Contig23"

```

misc.feature 176291..202324
/Note="assembly name:Contig23"
BASE COUNT 56787 a 45300 c 43765 g 54528 t 1944 others
ORIGIN

Query Match 20.1%; Score 137; DB 2; Length 202324;
Best Local Similarity 100.0%; Pred. No. 1e-64;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 495 atttgaaacctatggaacatctatgataatgcccaatgtgaagatggaatgaat 554
|||||
DB 83498 ATTGTAAACCTTATGTGACAAATCCTATTATATGATGCCCAATGTGAAGATGGCAATGAAT 83439

QY 555 aatggaagaatgaacggagatcgcaacattttgataagaagtataagaacctattga 614
|||||
DB 83438 AATGGAAGTGAACGGGATGCGCCAACTTTGTGATTAAGAAGATTATGAAGCCATTATTGA 83379

QY 615 agaccttaagaagaag 631
|||||
DB 83378 AGACCTTAAGAAGAAG 83362

RESULT 7
AK021919 2056 bp mRNA PRI 29-SEP-2000
LOCUS Homo sapiens CDNA FLJ11857 fis, clone HEMBA1006807, moderately
DEFINITION similar to Homo sapiens mRNA for SPOR.
ACCESSION AK021919.1 GI:10433216
VERSION AK021919.1
KEYWORDS oligo capping; fis (full insert sequence);
SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head CDNA to
mRNA, clone lib:HEMBA1 clone:HEMBA1006807.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
Tanase,T., Nomura,Y., Todoya,S., Komai,F., Hara,R., Takeuchi,K.,
Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuno,Y. and Oshima,A.
NEDO human CDNA sequencing project
Unpublished (2000)
2 (bases 1 to 2056)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao
Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,
Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT NEDO human CDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection;
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
FEATURES
source
1..2056
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1006807"
/clone_lib="HEMBA1"
/dev_stage="embryo, 10 weeks"
/tissue_type="whole embryo, mainly head"
/note="cloning vector: PME185FL3"
247..1422
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB13937.1"
/db_xref="GI:10433217"
/translation="MSRREPTPLPGDMSTGPIAESWCYQVAVKVFYSYMTINNFSC

```

```

REMEGEVLKSTPSSGSPDKMKCLRVNPKGIDSKDYLSLYLLVSPKSEVRAPK
KSLINAKREETKAMESORAYFEVQKDMGFKFTIRPDLDEANGLDLDDKLTJCE
VSVODDSVNSGHTNTNTLKVPECEPLAEDGLMNTRETDGCSFPRGQFEAKHSVL
AARSPVPNAMPHEMBEBSKKNVEIENDLDPYFKEMKRPITYGRAPNDDKADNLLAA
ADKVALDERKVCERALCNSLSEVENAVDTLVADLHSAEQLAQAIDFLNRCVLRQL
GCKDKRMSNSNQTIDIMESERDRHFDEKVMKAYIEDLKERESVPSYTTKVSFSLQ"
BASE COUNT 642 a 394 c 495 g 525 t
ORIGIN

Query Match 18.9%; Score 129; DB 9; Length 2056;
Best Local Similarity 100.0%; Pred. No. 2.5e-60;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 553 atraatgaagaatgaacggagatcgcaacattttgataagaagtataagaacctatt 612
|||||
DB 1294 ATATGGAAGTGAACGGGATGCGCCAACTTTGATTAAGAAGTTATGAAGCCTTATT 1353

QY 613 gaagaccttaagaagaagaatctgtccagctataccaccagaatgtctttaagcct 672
|||||
DB 1354 GAAGACCTTAAGAAGAAGATCTGTCCAGCTATACCAACCAAGTGTCTTTAGCCTT 1413

QY 673 caactttga 681
|||||
DB 1414 CAACCTTTGA 1422

RESULT 8
AC013467/c 172966 bp DNA PRI 25-MAY-2001
LOCUS AC013467/c
DEFINITION Homo sapiens clone RP11-451F14, complete sequence.
ACCESSION AC013467
VERSION AC013467.8 GI:14196420
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 172966)
Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (bases 1 to 172966)
Waterston,R.H.
Direct Submission
Submitted (25-MAY-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On May 25, 2001 this sequence version replaced gi:13624417.
Center Project name: H.NH0451F14.
FEATURES
source
1..172966
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-451F14"
BASE COUNT 57371 a 34327 c 31782 g 49486 t
ORIGIN

Query Match 5.3%; Score 36; DB 9; Length 172966;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 gtagatatcagcaacaagttttccagtggtccca 255
|||||
DB 168708 GTAGATATCTACGACCAAGATTTCACAGTGCCCA 168673

```

RESULT 9
AC025574 155929 bp DNA HTG 06-SEP-2000
LOCUS Homo sapiens chromosome 12 clone RP11-348M3, WORKING DRAFT
DEFINITION SQUENCE, 14 unordered pieces.
AC025574
VERSION AC025574.10 GI:9438393
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 155929)
Muzny,D.M., Adams,C., Bailey,M., Barbara,J., Blankenburg,K.,
Bodot,A., Boucek,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
Burbett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N.,
Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
Forcum-Tansey,J., Frantz,P., Ganesha,R., Gorrell,J.H., Gorrell,L.L.,
Guevara,M., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,
Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M.,
Kelly,S., Kondolewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z.,
Lichter,O., Liu,J., Liu,W., Logan,O., Lozano,R.J., Lu,J.,
Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mel,G., Morgan,M.,
Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S.,
Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L.,
Quiles,M., Relter,D., Rives,M., Samuel,S., Say,J., Scherer,S.,
Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sucgang,R.,
Taber,P., Taylor,T., Vasquez,L., Vinson,R., Vo,O., Wahbah,M.,
Watlington,S., Weinstein,G., Weinstein,I.R., Williamson,A.,
Worley,K., Wren,J., Wrenford,G., Yu,W., Zhou,X., Nelson,D. and
Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 155929)
Worley,K.C.
Submitted (11-MAR-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 25, 2000 this sequence version replaced gi:8571540.
COMMENT
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HAIT
Center clone name: RP11-348M3
----- Summary Statistics
Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye; 94% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 133622 bases at least Q40
Consensus quality: 145733 bases at least Q30
Consensus quality: 150334 bases at least Q20
Estimated insert size: 150694; sum-of-coverage estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 3.9x in Q20 bases; sum-of-coverage estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 36972: contig of 36972 bp in length

FEATURES
source
1..155929
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-348M3"
Location/Qualifiers
*
* 36973 37072: gap of unknown length
* 37073 64901: contig of 27829 bp in length
* 64902 65001: gap of unknown length
* 65002 91014: contig of 26013 bp in length
* 91015 91114: gap of unknown length
* 91115 105122: contig of 14008 bp in length
* 105123 105222: gap of unknown length
* 105223 113963: contig of 8741 bp in length
* 113964 124894: gap of unknown length
* 124895 124994: gap of unknown length
* 124995 132612: contig of 7618 bp in length
* 132613 132712: gap of unknown length
* 132713 139659: contig of 6947 bp in length
* 139660 139759: gap of unknown length
* 139760 143764: contig of 4005 bp in length
* 143765 143864: gap of unknown length
* 143865 148062: contig of 4198 bp in length
* 148063 148162: gap of unknown length
* 148163 151000: contig of 2838 bp in length
* 151001 151100: gap of unknown length
* 151101 153374: contig of 2274 bp in length
* 153375 153474: gap of unknown length
* 153475 154810: contig of 1336 bp in length
* 154811 154910: gap of unknown length
* 154911 155929: contig of 1019 bp in length.
BASE COUNT 40876 a 36387 c 36205 g 41119 t 1342 others
ORIGIN
Query Match 3.28; Score 22; DB 2; Length 155929;
Best Local Similarity 100.0%; Pred. No. 1,1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 464 ctgcccttgactcatccac 485
|||||
Db 154274 CTGCCCTTGACTCATCCAC 154295
RESULT 10
AC090521 77644 bp DNA INV 27-FEB-2001
LOCUS Caenorhabditis briggsae cosmid CB002D19, complete sequence.
DEFINITION AC090521
AC090521
VERSION AC090521.1 GI:13129524
KEYWORDS HTG.
SOURCE Caenorhabditis briggsae.
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peleiderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 77644)
AUTHORS Washington University Genome Sequencing Center.
TITLE The C. briggsae Genome Sequencing Project
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 77644)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA
e-mail: jsp@ethewatson.wustl.edu

NOTICE: This sequence may not be the entire insert of this clone.

It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

FEATURES
source
Location/Qualifiers
1..77644

/organism="Caenorhabditis briggsae"
/strain="Gujarat G16"
/db_xref="taxon:6238"
/clone="CB002D19"
64453..64525
/note="codon recognized: AAA"
/product="tRNA-Lys"
BASE COUNT 22191 a 14948 c 15587 g 24918 t
ORIGIN

Query Match 3.1%; Score 21; DB 3; Length 77644;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ctgccaaaacccaatctca 36
|||||
Db 62656 CTGCCAAAACCAATCTCA 62676

RESULT 11
AC011381 109549 bp DNA HTG 23-APR-2001
LOCUS
DEFINITION Homo sapiens chromosome 5 clone CTB-133N3, WORKING DRAFT SEQUENCE,
7 unordered pieces.
AC011381
AC011381.5 GI:8576058
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 109549)
JOURNAL DOE Joint Genome Institute.
REFERENCE
AUTHORS Unpublished
TITLE 2 (bases 1 to 109549)
JOURNAL DOE Joint Genome Institute.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Jun 21, 2000 this sequence version replaced gi:7710349.

-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov.

Project Information
Center Project Name: 115591, H239
Center clone name: CIT9785KB_133N3

Summary Statistics
Consensus quality: 98174 bases at least Q40
Consensus quality: 103469 bases at least Q30
Consensus quality: 105214 bases at least Q20
Estimated insert size: 110000; pulse field gel estimation
Estimated insert size: 108949; sum-of-contigs estimation
Quality coverage: 5.98 in Q20 bases; pulse field gel estimation
Quality coverage: 6.04 in Q20 bases; sum-of-contigs estimation
NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1231: contig of 1231 bp in length

* 1232 1331: gap of unknown length
* 1332 8134: contig of 6803 bp in length
* 8135 8234: gap of unknown length
* 8235 15598: contig of 7364 bp in length
* 15599 15698: gap of unknown length
* 15699 22852: contig of 7154 bp in length
* 22853 30470: gap of unknown length
* 30471 30570: contig of 7518 bp in length
* 30571 59501: gap of unknown length
* 59502 59601: contig of 28931 bp in length
* 59602 109549: gap of unknown length
* 109549: contig of 49948 bp in length.
location/Qualifiers
1..109549
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTB-133N3"
/clone_lib="Caltech human BAC library B"
BASE COUNT 31123 a 25360 c 23787 g 28626 t 653 others
ORIGIN

Query Match 3.1%; Score 21; DB 2; Length 109549;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 578 aacatttgataagaagta 598
|||||
Db 109083 AACATTGTGATPAAAGAGTTA 109103

RESULT 12
AC004821/c 163332 bp DNA PRI 16-NOV-2000
LOCUS
DEFINITION Homo sapiens clone RPI-98022, complete sequence.
AC004821
AC004821.3 GI:11181836
VERSION
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 163332)
JOURNAL Waterston, R.H.
REFERENCE
AUTHORS Unpublished
TITLE 2 (bases 1 to 163332)
JOURNAL Waterston, R.H.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (12-JUN-1998) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
COMMENT MO 63108, USA
On Nov 16, 2000 this sequence version replaced gi:4753291.

Project Information
Center Project Name: 115591, H239
Center clone name: CIT9785KB_133N3

Summary Statistics
Consensus quality: 98174 bases at least Q40
Consensus quality: 103469 bases at least Q30
Consensus quality: 105214 bases at least Q20
Estimated insert size: 110000; pulse field gel estimation
Estimated insert size: 108949; sum-of-contigs estimation
Quality coverage: 5.98 in Q20 bases; pulse field gel estimation
Quality coverage: 6.04 in Q20 bases; sum-of-contigs estimation
NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1231: contig of 1231 bp in length

```

source
1. 163332
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP1-98022"

BASE COUNT      44502 a 38204 c 37986 g 42640 t
ORIGIN

Query Match      3.1%; Score 21; DB 9; Length 163332;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 578 aacatttgataagaagatga 598
|||||
Db 4554 AACATTTCATTAAGAGAGTTA 4534

RESULT 13
AC016521 180541 bp DNA HTG 13-DEC-2000
LOCUS Homo sapiens clone RP11-29F8, WORKING DRAFT SEQUENCE, 17 unordered
DEFINITION
AC016521
AC016521 4 GI:11693419
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 180541)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
2 (bases 1 to 180541)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heathford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehocky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McMan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Teefaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 13, 2000 this sequence version replaced g1:1181822.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information
Center project name: L4829
Center clone name: 29_F_8
----- Summary Statistics
Sequencing vector: M13; M77815; 3% of reads
Sequencing vector: Plasmid; n/a; 97% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 174572 bases at least Q40
Consensus quality: 177046 bases at least Q30
Consensus quality: 178064 bases at least Q20
Insert size: 184000; agarose-fp
Insert size: 178941; sum-of-ctrls

```

```

FEATURES
source
1. 180541
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-29F8"
/clone_lib="RP11-29F8"
Location/Qualifiers
1. 862
/note="assembly_fragment"
clone_end:SP6
vector_side:left"
963. 1717
/note="assembly_fragment"
1818. 3133
/note="assembly_fragment"
3234. 4640
/note="assembly_fragment"
4741. 8634
/note="assembly_fragment"
8735. 10546
/note="assembly_fragment"
10647. 13769
/note="assembly_fragment"
13870. 17470
/note="assembly_fragment"
17571. 22684
/note="assembly_fragment"
22785. 31278
/note="assembly_fragment"
31379. 43626
/note="assembly_fragment"

```

Quality coverage: 6.9 in Q20 bases; agarose-fp
 Quality coverage: 7.1 in Q20 bases.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 17 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1
863 962: gap of 100 bp
963 1717: contig of 755 bp in length
1718 1817: gap of 100 bp
1818 3133: contig of 1316 bp in length
3134 3233: gap of 100 bp
3234 4640: contig of 1407 bp in length
4641 4740: gap of 100 bp
4741 8634: contig of 3894 bp in length
8635 8734: gap of 100 bp
8735 10546: contig of 1812 bp in length
10547 10646: gap of 100 bp
10647 13769: contig of 3123 bp in length
13770 13869: gap of 100 bp
13870 17470: contig of 3601 bp in length
17471 17570: gap of 100 bp
17571 22684: contig of 5114 bp in length
22685 22784: gap of 100 bp
22785 31278: contig of 8494 bp in length
31279 31378: gap of 100 bp
31379 43626: contig of 12248 bp in length
43627 43726: gap of 100 bp
43727 56284: contig of 12558 bp in length
56285 56384: gap of 100 bp
56385 66809: contig of 10425 bp in length
66810 66909: gap of 100 bp
66910 86271: contig of 19362 bp in length
86272 86371: gap of 100 bp
86372 103947: contig of 17576 bp in length
103948 104047: gap of 100 bp
104048 137483: contig of 33436 bp in length
137484 137583: gap of 100 bp
137584 180541: contig of 42958 bp in length.

```

misc_feature	43727. 456284
misc_feature	/note="assembly_fragment"
misc_feature	56385. 66809
misc_feature	/note="assembly_fragment"
misc_feature	66910. 86271
misc_feature	/note="assembly_fragment"
misc_feature	86372. 103947
misc_feature	/note="assembly_fragment"
misc_feature	104048. 137483
misc_feature	/note="assembly_fragment"
misc_feature	137584. 180541

	vector_side:right"									
BASE COUNT	50954	a	38430	c	39265	g	50267	t	1625	others
ORIGIN										

Query Match	3.1%	Score 21	DB 2	Length 180541
Best Local Similarity	100.0%	Pred. No. 4		
Matches 21	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```
QY      338  ggctagagagctgcagagct  358
          |||||
Db 49823  GGCTAGAGAGCTGCAGAGCT  49843
```

RESULT	14
LOCUS	AC022182
DEFINITION	AC022182 193379 bp DNA
ACCESSION	Homo sapiens chromosome 8 clone RP11-174G1 map 8,
VERSION	PROGRESS ***, 71 unordered pieces.
KEYWORDS	AC022182
SOURCE	AC022182.3 GI:7143437
ORGANISM	HTG; HTGS_PPHASEL.
	human.
	Homo sapiens
	03-MAR-2000
	*** SEQUENCING IN

```
----- Project Information
Center project name: L2078
Center clone name: 174_G_1
```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 71 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

* 44227 44326: gap of 100 bp
* 44327 45918: contig of 1592 bp in length
* 45919 46018: gap of 100 bp
* 46019 47637: contig of 1619 bp in length
* 47638 47737: gap of 100 bp
* 47738 49872: contig of 2135 bp in length
* 49873 49972: gap of 100 bp
* 49973 52711: contig of 2739 bp in length
* 52712 52811: gap of 100 bp
* 52812 55253: contig of 2442 bp in length
* 55254 55353: gap of 100 bp
* 55354 56537: contig of 1184 bp in length
* 56538 56637: gap of 100 bp
* 56638 58784: contig of 2147 bp in length
* 58785 58884: gap of 100 bp
* 58885 61009: contig of 2125 bp in length
* 61010 61109: gap of 100 bp
* 61110 63658: contig of 2549 bp in length
* 63659 63758: gap of 100 bp
* 63759 64988: contig of 1230 bp in length
* 64989 65088: gap of 100 bp
* 65089 66555: contig of 1467 bp in length
* 66556 66655: gap of 100 bp
* 66656 69110: contig of 2455 bp in length
* 69111 69210: gap of 100 bp
* 69211 71149: contig of 1939 bp in length
* 71150 71249: gap of 100 bp
* 71250 73237: contig of 1988 bp in length
* 73238 73337: gap of 100 bp
* 73338 76363: contig of 3026 bp in length
* 76364 76463: gap of 100 bp
* 76464 78717: contig of 2254 bp in length
* 78718 78817: gap of 100 bp
* 78818 81222: contig of 2405 bp in length
* 81223 81322: gap of 100 bp
* 81323 84081: contig of 2759 bp in length
* 84082 84181: gap of 100 bp
* 84182 87362: contig of 3181 bp in length
* 87363 87462: gap of 100 bp
* 87463 91079: contig of 3617 bp in length
* 91080 91179: gap of 100 bp
* 91180 94730: contig of 3551 bp in length
* 94731 94830: gap of 100 bp
* 94831 98146: contig of 3316 bp in length
* 98147 98246: gap of 100 bp
* 98247 102034: contig of 3788 bp in length
* 102035 102134: gap of 100 bp
* 102135 105763: contig of 3629 bp in length
* 105764 105863: gap of 100 bp
* 105864 108749: contig of 2886 bp in length
* 108750 108849: gap of 100 bp
* 108850 113126: contig of 4277 bp in length
* 113127 113226: gap of 100 bp
* 113227 117652: contig of 4426 bp in length
* 117653 117752: gap of 100 bp
* 117753 121602: contig of 3850 bp in length
* 121603 121702: gap of 100 bp
* 121703 126141: contig of 4439 bp in length
* 126142 126241: gap of 100 bp
* 126242 130579: contig of 4338 bp in length
* 130580 130679: gap of 100 bp
* 130680 134477: contig of 3798 bp in length
* 134478 134577: gap of 100 bp
* 134578 141667: contig of 7090 bp in length
* 141668 141767: gap of 100 bp
* 141768 147874: contig of 6107 bp in length
* 147875 147974: gap of 100 bp
* 147975 153773: contig of 5799 bp in length
* 153774 153873: gap of 100 bp
* 153874 160439: contig of 6566 bp in length
* 160440 160539: gap of 100 bp
* 160540 166630: contig of 6091 bp in length
* 166631 166730: gap of 100 bp

```

```

* 166731 174571: contig of 7841 bp in length
* 174572 174671: gap of 100 bp
* 174672 180128: contig of 5457 bp in length
* 180129 180228: gap of 100 bp
* 180229 186362: contig of 6134 bp in length
* 186363 186462: gap of 100 bp
* 186463 193379: contig of 6917 bp in length.
Location/Qualifiers
1. .193379
/organism="Homo sapiens"

```

```

Query Match 3 1%: Score 21; DB 2; Length 193379;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 338 ggcctagagagctgcagagct 358
|||||
Db 181205 GGCTAGAGAGCTGCAGAGCT 181225

```

```

RESULT 15
RP282365 410 bp DNA BCT 07-MAR-1997
LOCUS RP282365/C
DEFINITION R. prowazekii genomic DNA fragment (clone A336R).
ACCESSION Z62365
VERSION Z62365.1 GI:1871716
KEYWORDS
SOURCE
ORGANISM
Rickettsia prowazekii.
Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiaceae; Rickettsia; typhus group.
1 (bases 1 to 410)
Anderson, S.G., Eriksson, A.S., Naslund, A.K., Andersen, M.S. and
Kurland, C.G.
The Rickettsia prowazekii genome: a random sequence analysis
Microb. Comp. Genomics 1 (4), 293-315 (1996)
9853639
2 (bases 1 to 410)
Anderson, S.G.E.
Direct Submission
Submitted (31-OCT-1996) Anderson, S.G.E., Department of Molecular
Biology, Husegatan 3, BOX 590, Biomedical Center, S-751 24
Uppsala, SWEDEN
The overall error rate is an estimated 0.5%.

```

```

COMMENT
FEATURES
source
Location/Qualifiers
1. .410
/organism="Rickettsia prowazekii"
/strain="Madrid E"
/db_xref="taxon:782"
/clone_lib="genomic DNA, J. Bacteriol.
177:4171-4175(1995)"
/clone="A336R"

```

```

BASE COUNT 93 a 66 c 84 g 165 t 2 others
ORIGIN

```

```

Query Match 2.9%; Score 20; DB 1; Length 410;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 482 ccacaccttaaatgtgta 501
|||||
Db 358 CCACACCTTAAATTTGTA 339

```

```

Search completed: February 26, 2002, 13:28:46
Job time: 9657 sec

```